

## SEQUENCE LISTING

<110> Giese, Klaus  
Xin, Hong

<120> METASTATIC BREAST AND COLON CANCER REGULATED GENES

<130> 1451.002 / 210030.447

<140> US 09/215,450

<141> 1998-12-17

<160> 27

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 2429

<212> DNA

<213> human

<400> 1

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&lt;211&gt; 486

&lt;212&gt; DNA

&lt;213&gt; human

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(486)

&lt;223&gt; n = A,T,C or G

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catttcctcc caaatttctg ggattacagg cttaagctac cacacctggc cagccctcaa	360
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&lt;211&gt; 397

&lt;212&gt; DNA

&lt;213&gt; human

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(397)

&lt;223&gt; n = A,T,C or G

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&lt;210&gt; 4

&lt;211&gt; 376

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 <213> human

<400> 4

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<210> 5  
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 <212> DNA  
 <213> human

<400> 5

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<400> 6

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 <211> 218  
 <212> DNA  
 <213> human

<220>  
 <221> misc\_feature  
 <222> (1) ... (218)  
 <223> n = A,T,C or G

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ccgagacaat ataaatgtac aatggatacc cgatgcaaac aatgtattgt ggttaactag	180
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 <211> 426  
 <212> DNA  
 <213> human

<220>  
 <221> misc\_feature  
 <222> (1) ... (426)  
 <223> n = A,T,C or G

<400> 8

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<211> 442

<212> DNA

<213> human

<400> 12

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<211> 332

<212> DNA

<213> human

<220>

<221> misc\_feature

<222> (1)...(332)

<223> n = A,T,C or G

<400> 13

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gtatacgtgt	aagaatgcct	ttattattca	atcagacatt	agggtctaag	aaaacccagg	240
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<210> 14

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<212> DNA

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<220>

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&lt;222&gt; (1)...(970)

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&lt;400&gt; 14

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tatggtaggc	aactaacgg	gttttaagg	gggtcta	ctgcctttc	aatgattta	900
ttggatttt	tttatccgc	aaatctctt	agtaacaaca	cattaagtgt	gaattacttt	960
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&lt;210&gt; 15

&lt;211&gt; 528

&lt;212&gt; DNA

&lt;213&gt; human

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(528)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 15

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&lt;210&gt; 16

&lt;211&gt; 3831

&lt;212&gt; DNA

&lt;213&gt; human

&lt;400&gt; 16

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&lt;210&gt; 19

&lt;211&gt; 518

&lt;212&gt; PRT

&lt;213&gt; human

&lt;400&gt; 19

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							20		25			30			
Leu	Arg	Val	Ala	Ala	Ala	Thr	Asn	Arg	Val	Val	Ala	Pro	Thr	Pro	Gly
							35		40			45			
Pro	Gly	Thr	Pro	Ala	Glu	Arg	His	Ala	Asp	Gly	Leu	Ala	Leu		
							50		55			60			
Glu	Pro	Ala	Leu	Ala	Ser	Pro	Ala	Gly	Ala	Ala	Asn	Phe	Leu	Ala	Met
							65		70			75			80
Val	Asp	Asn	Leu	Gln	Gly	Asp	Ser	Gly	Arg	Gly	Tyr	Tyr	Leu	Glu	Met
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Tyr	Phe	Asp	Thr	Glu	Arg	Ser	Ser	Thr	Tyr	Arg	Ser	Lys	Gly	Phe	Asp
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Val	Thr	Val	Lys	Tyr	Thr	Gln	Gly	Ser	Trp	Thr	Gly	Phe	Val	Gly	Glu
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Trp Asn Gly Ile Leu Gly Leu Ala	Tyr Ala Thr Leu Ala	Lys Pro Ser	
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Ser Ser Leu Glu Thr Phe Phe Asp Ser	Leu Val Thr Gln Ala Asn Ile		
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Pro Asn Val Phe Ser Met Gln Met Cys	Gly Ala Gly Leu Pro Val Ala		
225	230	235	240
Gly Ser Gly Thr Asn Gly Gly Ser	Leu Val Leu Gly Gly Ile Glu Pro		
245	250	255	
Ser Leu Tyr Lys Gly Asp Ile Trp Tyr	Thr Pro Ile Lys Glu Glu Trp		
260	265	270	
Tyr Tyr Gln Ile Glu Ile Leu Lys	Leu Glu Ile Gly Gly Gln Ser Leu		
275	280	285	
Asn Leu Asp Cys Arg Glu Tyr Asn Ala Asp	Lys Ala Ile Val Asp Ser		
290	295	300	
Gly Thr Thr Leu Leu Arg Leu Pro Gln	Lys Val Phe Asp Ala Val Val		
305	310	315	320
Glu Ala Val Ala Arg Ala Ser Leu Ile	Pro Glu Phe Ser Asp Gly Phe		
325	330	335	
Trp Thr Gly Ser Gln Leu Ala Cys	Trp Thr Asn Ser Glu Thr Pro Trp		
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Ser Tyr Phe Pro Lys Ile Ser Ile	Tyr Leu Arg Asp Glu Asn Ser Ser		
355	360	365	
Arg Ser Phe Arg Ile Thr Ile Leu Pro	Gln Leu Tyr Ile Gln Pro Met		
370	375	380	
Met Gly Ala Gly Leu Asn Tyr Glu	Cys Tyr Arg Phe Gly Ile Ser Pro		
385	390	395	400
Ser Thr Asn Ala Leu Val Ile Gly	Ala Thr Val Met Glu Gly Phe Tyr		
405	410	415	
Val Ile Phe Asp Arg Ala Gln	Lys Arg Val Gly Phe Ala Ala Ser Pro		
420	425	430	
Cys Ala Glu Ile Ala Gly Ala	Ala Val Ser Glu Ile Ser Gly Pro Phe		
435	440	445	
Ser Thr Glu Asp Val Ala Ser Asn	Cys Val Pro Ala Gln Ser Leu Ser		
450	455	460	
Glu Pro Ile Leu Trp Ile Val Ser	Tyr Ala Leu Met Ser Val Cys Gly		
465	470	475	480
Ala Ile Leu Leu Val Ile Val Leu	Leu Leu Leu Pro Phe Arg Cys		
485	490	495	
Gln Arg Arg Pro Arg Asp Pro	Glu Val Val Asn Asp Glu Ser Ser Leu		
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Val Arg His Arg Trp Lys			
515			

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&lt;211&gt; 31

&lt;212&gt; DNA

&lt;213&gt; human

&lt;400&gt; 20

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 Lys Lys Lys Leu Arg Ala Arg Ser Gln Leu Ser Glu Phe Trp Lys Ser  
 35 40 45  
 His Asn Leu Asp Met Ile Gln Phe Thr Glu Ser Cys Ser Met Asp Gln  
 50 55 60  
 Ser Ala Lys Glu Pro Leu Ile Asn Tyr Leu Asp Met Glu Tyr Phe Gly  
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 Ala Cys Lys Thr His Ser Arg Phe Gln Pro Ser Gln Ser Ser Thr Tyr  
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 260 265 270  
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 275 280 285  
 Gly Pro Ser Asp Lys Ile Lys Gln Leu Gln Asn Ala Ile Gly Ala Ala  
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 Pro Val Asp Gly Glu Tyr Ala Val Glu Cys Ala Asn Leu Asn Val Met  
 305 310 315 320

Pro Asp Val Thr Phe Thr Ile Asn Gly Val Pro Tyr Thr Leu Ser Pro  
 325 330 335  
 Thr Ala Tyr Thr Leu Leu Asp Phe Val Asp Gly Met Gln Phe Cys Ser  
 340 345 350  
 Ser Gly Phe Gln Gly Leu Asp Ile His Pro Pro Ala Gly Pro Leu Trp  
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 50 55 60  
 Glu Gln Pro Leu Glu Asn Tyr Leu Asp Met Glu Tyr Phe Gly Thr Ile  
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 225 230 235 240  
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 245 250 255  
 Asp Ser Ile Thr Met Asn Gly Glu Ala Ile Ala Cys Ala Glu Gly Cys  
 260 265 270  
 Gln Ala Ile Val Asp Thr Gly Thr Ser Leu Leu Thr Gly Pro Thr Ser  
 275 280 285

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 Gly Asp Met Val Val Ser Cys Ser Ala Ile Ser Ser Leu Pro Asp Ile  
 305 310 315 320  
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 325 330 335  
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 Leu Pro Thr Glu Ser Gly Glu Leu Trp Ile Leu Gly Asp Val Phe Ile  
 355 360 365  
 Arg Gln Tyr Phe Thr Val Phe Asp Arg Ala Asn Asn Gln Val Gly Leu  
 370 375 380  
 Ala Pro Val Ala  
 385

<210> 24  
 <211> 388  
 <212> PRT  
 <213> Homo sapien

<400> 24  
 Met Lys Trp Met Val Val Leu Val Cys Leu Gln Leu Leu Glu Ala  
 1 5 10 15  
 Ala Val Val Lys Val Pro Leu Lys Lys Phe Lys Ser Ile Arg Glu Thr  
 20 25 30  
 Met Lys Glu Lys Gly Leu Leu Gly Glu Phe Leu Arg Thr His Lys Tyr  
 35 40 45  
 Asp Pro Ala Trp Lys Tyr Arg Phe Gly Asp Leu Ser Val Thr Tyr Glu  
 50 55 60  
 Pro Met Ala Tyr Met Asp Ala Ala Tyr Phe Gly Glu Ile Ser Ile Gly  
 65 70 75 80  
 Thr Pro Pro Gln Asn Phe Leu Val Leu Phe Asp Thr Gly Ser Ser Asn  
 85 90 95  
 Leu Trp Val Pro Ser Val Tyr Cys Gln Ser Gln Ala Cys Thr Ser His  
 100 105 110  
 Ser Arg Phe Asn Pro Ser Glu Ser Ser Thr Tyr Ser Thr Asn Gly Gln  
 115 120 125  
 Thr Phe Ser Leu Gln Tyr Gly Ser Gly Ser Leu Thr Gly Phe Phe Gly  
 130 135 140  
 Tyr Asp Thr Leu Thr Val Gln Ser Ile Gln Val Pro Asn Gln Glu Phe  
 145 150 155 160  
 Gly Leu Ser Glu Asn Glu Pro Gly Thr Asn Phe Val Tyr Ala Gln Phe  
 165 170 175  
 Asp Gly Ile Met Gly Leu Ala Tyr Pro Ala Leu Ser Val Asp Glu Ala  
 180 185 190  
 Thr Thr Ala Met Gln Gly Met Val Gln Glu Gly Ala Leu Thr Ser Pro  
 195 200 205  
 Val Phe Ser Val Tyr Leu Ser Asn Gln Gln Gly Ser Ser Gly Gly Ala  
 210 215 220  
 Val Val Phe Gly Gly Val Asp Ser Ser Leu Tyr Thr Gly Gln Ile Tyr  
 225 230 235 240  
 Trp Ala Pro Val Thr Gln Glu Leu Tyr Trp Gln Ile Gly Ile Glu Glu  
 245 250 255  
 Phe Leu Ile Gly Gly Gln Ala Ser Gly Trp Cys Ser Glu Gly Cys Gln

260	265	270
Ala Ile Val Asp Thr Gly Thr Ser	Leu Leu Thr Val Pro Gln Gln Tyr	
275	280	285
Met Ser Ala Leu Leu Gln Ala Thr Gly Ala Gln Glu Asp Glu Tyr Gly		
290	295	300
Gln Phe Leu Val Asn Cys Asn Ser Ile Gln Asn Leu Pro Ser Leu Thr		
305	310	315
Phe Ile Ile Asn Gly Val Glu Phe Pro Leu Pro Pro Ser Ser Tyr Ile		
325	330	335
Leu Ser Asn Asn Gly Tyr Cys Thr Val Gly Val Glu Pro Thr Tyr Leu		
340	345	350
Ser Ser Gln Asn Gly Gln Pro Leu Trp Ile Leu Gly Asp Val Phe Leu		
355	360	365
Arg Ser Tyr Tyr Ser Val Tyr Asp Leu Gly Asn Asn Arg Val Gly Phe		
370	375	380
Ala Thr Ala Ala		
385		

<210> 25  
 <211> 412  
 <212> PRT  
 <213> Homo sapien

<400> 25		
Met Gln Pro Ser Ser Leu Leu Pro Leu Ala Leu Cys Leu Leu Ala Ala		
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Pro Ala Ser Ala Leu Val Arg Ile Pro Leu His Lys Phe Thr Ser Ile		
20	25	30
Arg Arg Thr Met Ser Glu Val Gly Gly Ser Val Glu Asp Leu Ile Ala		
35	40	45
Lys Gly Pro Val Ser Lys Tyr Ser Gln Ala Val Pro Ala Val Thr Glu		
50	55	60
Gly Pro Ile Pro Glu Val Leu Lys Asn Tyr Met Asp Ala Gln Tyr Tyr		
65	70	75
Gly Glu Ile Gly Ile Gly Thr Pro Pro Gln Cys Phe Thr Val Val Phe		
85	90	95
Asp Thr Gly Ser Ser Asn Leu Trp Val Pro Ser Ile His Cys Lys Leu		
100	105	110
Leu Asp Ile Ala Cys Trp Ile His His Lys Tyr Asn Ser Asp Lys Ser		
115	120	125
Ser Thr Tyr Val Lys Asn Gly Thr Ser Phe Asp Ile His Tyr Gly Ser		
130	135	140
Gly Ser Leu Ser Gly Tyr Leu Ser Gln Asp Thr Val Ser Val Pro Cys		
145	150	155
Gln Ser Ala Ser Ser Ala Ser Ala Leu Gly Gly Val Lys Val Glu Arg		
165	170	175
Gln Val Phe Gly Glu Ala Thr Lys Gln Pro Gly Ile Thr Phe Ile Ala		
180	185	190
Ala Lys Phe Asp Gly Ile Leu Gly Met Ala Tyr Pro Arg Ile Ser Val		
195	200	205
Asn Asn Val Leu Pro Val Phe Asp Asn Leu Met Gln Gln Lys Leu Val		
210	215	220
Asp Gln Asn Ile Phe Ser Phe Tyr Leu Ser Arg Asp Pro Asp Ala Gln		

225	230	235	240												
Pro	Gly	Gly	Glu	Leu	Met	Leu	Gly	Gly	Thr	Asp	Ser	Lys	Tyr	Tyr	Lys
					245					250					255
Gly	Ser	Leu	Ser	Tyr	Leu	Asn	Val	Thr	Arg	Lys	Ala	Tyr	Trp	Gln	Val
					260			265							270
His	Leu	Asp	Gln	Val	Glu	Val	Ala	Ser	Gly	Leu	Thr	Leu	Cys	Lys	Gl
					275			280							285
Gly	Cys	Glu	Ala	Ile	Val	Asp	Thr	Gly	Thr	Ser	Leu	Met	Val	Gly	Pro
					290			295							300
Val	Asp	Glu	Val	Arg	Glu	Leu	Gln	Lys	Ala	Ile	Gly	Ala	Val	Pro	Leu
					305			310			315				320
Ile	Gln	Gly	Glu	Tyr	Met	Ile	Pro	Cys	Glu	Lys	Val	Ser	Thr	Leu	Pro
					325			330							335
Ala	Ile	Thr	Leu	Lys	Leu	Gly	Gly	Lys	Gly	Tyr	Lys	Leu	Ser	Pro	Gl
					340			345							350
Asp	Tyr	Thr	Leu	Lys	Val	Ser	Gln	Ala	Gly	Lys	Thr	Leu	Cys	Leu	Ser
					355			360							365
Gly	Phe	Met	Gly	Met	Asp	Ile	Pro	Pro	Pro	Ser	Gly	Pro	Leu	Trp	Ile
Leu	Gly	Asp	Val	Phe	Ile	Gly	Arg	Tyr	Tyr	Thr	Val	Phe	Asp	Arg	Asp
					385			390			395				400
Asn	Asn	Arg	Val	Gly	Phe	Ala	Glu	Ala	Ala	Arg	Leu				
					405					410					

<210> 26  
<211> 406  
<212> PRT  
<213> *Homo sapien*

<400> 26  
 Met Asp Gly Trp Arg Arg Met Pro Arg Trp Gly Leu Leu Leu Leu Leu  
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 Trp Gly Ser Cys Thr Phe Gly Leu Pro Thr Asp Thr Thr Phe Lys  
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 Arg Ile Phe Leu Lys Arg Met Pro Ser Ile Arg Glu Ser Leu Lys Glu  
 35 40 45  
 Arg Gly Val Asp Met Ala Arg Leu Gly Pro Glu Trp Ser Gln Pro Met  
 50 55 60  
 Lys Arg Leu Thr Leu Gly Asn Thr Thr Ser Ser Val Ile Leu Thr Asn  
 65 70 75 80  
 Tyr Met Asp Thr Gln Tyr Tyr Gly Glu Ile Gly Ile Gly Thr Pro Pro  
 85 90 95  
 Gln Thr Phe Lys Val Val Phe Asp Thr Gly Ser Ser Asn Val Trp Val  
 100 105 110  
 Pro Ser Ser Lys Cys Ser Arg Leu Tyr Thr Ala Cys Val Tyr His Lys  
 115 120 125  
 Leu Phe Asp Ala Ser Asp Ser Ser Ser Tyr Lys His Asn Gly Thr Glu  
 130 135 140  
 Leu Thr Leu Arg Tyr Ser Thr Gly Thr Val Ser Gly Phe Leu Ser Gln  
 145 150 155 160  
 Asp Ile Ile Thr Val Gly Gly Ile Thr Val Thr Gln Met Phe Gly Glu  
 165 170 175  
 Val Thr Glu Met Pro Ala Leu Pro Phe Met Leu Ala Glu Phe Asp Gly

180	185	190	
Val Val Gly Met Gly Phe Ile Glu Gln Ala Ile Gly Arg Val Thr Pro			
195	200	205	
Ile Phe Asp Asn Ile Ile Ser Gln Gly Val Leu Lys Glu Asp Val Phe			
210	215	220	
Ser Phe Tyr Tyr Asn Arg Asp Ser Glu Asn Ser Gln Ser Leu Gly Gly			
225	230	235	240
Gln Ile Val Leu Gly Gly Ser Asp Pro Gln His Tyr Glu Gly Asn Phe			
245	250	255	
His Tyr Ile Asn Leu Ile Lys Thr Gly Val Trp Gln Ile Gln Met Lys			
260	265	270	
Gly Val Ser Val Gly Ser Ser Thr Leu Leu Cys Glu Asp Gly Cys Leu			
275	280	285	
Ala Leu Val Asp Thr Gly Ala Ser Tyr Ile Ser Gly Ser Thr Ser Ser			
290	295	300	
Ile Glu Lys Leu Met Glu Ala Leu Gly Ala Lys Lys Arg Leu Phe Asp			
305	310	315	320
Tyr Val Val Lys Cys Asn Glu Gly Pro Thr Leu Pro Asp Ile Ser Phe			
325	330	335	
His Leu Gly Gly Lys Glu Tyr Thr Leu Thr Ser Ala Asp Tyr Val Phe			
340	345	350	
Gln Glu Ser Tyr Ser Ser Lys Lys Leu Cys Thr Leu Ala Ile His Ala			
355	360	365	
Met Asp Ile Pro Pro Pro Thr Gly Pro Thr Trp Ala Leu Gly Ala Thr			
370	375	380	
Phe Ile Arg Lys Phe Tyr Thr Glu Phe Asp Arg Arg Asn Asn Arg Ile			
385	390	395	400
Gly Phe Ala Leu Ala Arg			
405			

<210> 27

<211> 751

<212> DNA

<213> Homo sapien

<400> 27

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ttctcttctc tcttcaatct ctggaaaaat aagtacatat agttgataac ccctcttagc	180
ttacaggaag cttttgtat taattgcctt tgaggttatt ttccgcccaga cctcaacctg	240
ggtcaaagtg gtacagaag gcttgcagta tgatggcagg agaatcagcc tggggcctgg	300
ggatgttaacc aagctgtacc cttgagacct ggaaccagag ccacaggccc cttttgtggg	360
tttctctgtc ctctgaatgg gagccagaat tcactaggag gtcatcaacc gatggtcctc	420
acaaggctct tctgaagatg gaaggcctt tgcccgttga ggtagagggg aagggaaatct	480
cctctttgt acccaatact tatgttgtat tgttggtgcg aaagtaaaa cactacctct	540
tttggagactt tgccccagggt cctgtgcctg gatgggggtg caggcagcct tgaccacggc	600
tgtccccctc accccaaaaga attatcatcc caacagccaa gacccaaacag gtgctgaact	660
gtgcatcaac caggaagagt tctatccccca agctggccac tatcacatat gcttacttt	720
gcttaaaatt aataaatcat gtttgatga g	751